

**AMENDMENTS TO THE CLAIMS:**

This listing of claims will replace all prior versions, and listings of claims in the application:

**LISTING OF CLAIMS:**

**1-43. (canceled)**

**44. (withdrawn)** Mutated V1/AR1/AV1 or C1/AL1/AC1 gene sequence of a tomato infecting geminivirus wherein the mutations consist of point mutations distributed along the sequence in such a way that the continuous homology between the mutated sequence and the corresponding viral gene sequence is below or equal to 8 nucleotides, preferably below or equal to 5 nucleotides, said mutated sequence encoding for a capsid protein or for a Rep protein, respectively.

**45. (withdrawn)** Mutated V1/AR1/AV1 gene sequence according to claim 44, encoding for a capsid protein having sequence SEQ ID No 7.

**46. (withdrawn)** Mutated C1/AL1/AC1 gene sequence according to claim 44, wherein the mutation further comprises a truncation occurring at 3' terminal so that the mutated sequence encodes for a truncated Rep protein.

**47. (withdrawn)** Mutated C1/AL1 /AC1 gene sequences according to claim 46, wherein the truncated Rep proteins consist of 130 aminoacids (Rep 130) to 210 aminoacids (Rep 210).

**48. (withdrawn)** Mutated C1/AL1/AC1 gene sequence according to claim 46 encoding for Rep 210 SEQ ID No 3 or SEQ ID No 5.

**49. (withdrawn)** Mutated C1/AL1/AC1 gene sequence encoding for Rep 130 SEQ ID No 9.

**50. (withdrawn)** Mutated gene sequence according to claim 44 wherein the tomato infecting geminivirus is TYLCSV.

**51. (withdrawn)** Synthetic construct comprising an heterologous polynucleotide sequence containing in the 5'-3' direction:

a) polynucleotide sequence acting as promoter in said plant or tissue or transformed cells;

b) a non translated polynucleotide sequence positioned 5' of the encoding region;

c) a mutated gene sequence;

d) a sequence acting as transcription terminator, positioned 3' with respect to the mutated gene sequence.

**52. (withdrawn)** Expression vector comprising the construct as defined according to claim 51.

**53. (withdrawn)** Transgenic plant, tissue or plant cells thereof, comprising in their genome a mutated gene sequence according to claim 44.

**54. (withdrawn)** Seed comprising in its genome a mutated gene sequence according to claim 44.

**55. (currently amended)** A method for the preparation of transgenic plants, plant tissue or cells thereof having long lasting resistance against geminiviruses, including the following steps:

a) selection of a geminivirus ~~gene-derived~~ C1/AL1/AC1 polynucleotide sequence encoding an amino acid sequence ~~capable of~~ conferring resistance against geminiviruses, said resistance being overcome over time by geminivirus induced post-transcriptional transgene silencing;

b) mutagenesis of the selected geminivirus ~~gene-derived~~ C1/AL1/AC1 polynucleotide sequence, wherein the mutations consist of silent point mutations distributed along the geminivirus ~~gene-derived~~ C1/AL1/AC1 polynucleotide sequence so that continuous homology between the mutated C1/AL1/AC1 polynucleotide sequence and the ~~corresponding viral gene~~ selected C1/AL1/AC1

polynucleotide sequence is less than or equal to 8 nucleotides;  
and

c) insertion of the geminivirus ~~gene-derived~~ C1/AL1/AC1  
polynucleotide sequence mutated in the step b) in the plant,  
plant tissue or cell thereof, using a construct comprising an  
heterologous polynucleotide sequence containing in the 5'-3'  
direction:

i) a polynucleotide sequence acting as a promoter in said  
plant, plant tissue or cells;

ii) a non-translated polynucleotide sequence positioned 5'  
of the encoding region of the mutated geminivirus ~~gene-derived~~  
C1/AL1/AC1 polynucleotide sequence;

iii) a mutated C1/AL1/AC1 polynucleotide sequence  
mutagenised according to step (b) encoding a ~~mutagenised~~  
geminivirus-derived amino acid sequence, ~~mutagenised according to~~  
~~step (b) and capable to be~~ wherein the mutated C1/AL1/AC1  
polynucleotide sequence is an ineffective target of the  
geminivirus induced post-transcriptional transgene silencing; and

iv) a polynucleotide sequence acting as a transcription  
terminator positioned 3' with respect to said mutated C1/AL1/AC1  
polynucleotide sequence ~~encoding a mutagenised geminivirus-~~  
~~derived amino acid sequence.~~

56-57. (cancelled)

**58. (previously presented)** The method according to claim 55, wherein the geminiviruses are selected from the species belonging to the Begomovirus genus and isolates thereof.

**59. (previously presented)** The method according to claim 58, wherein the Begomoviruses species is Tomato yellow leaf curl Sardinia virus (TYLCSV).

**60-62. (cancelled)**

**63. (currently amended)** The method according to claim ~~61~~ 59, wherein the selected geminivirus-~~derived~~ C1/AL1/AC1 polynucleotide sequence ~~amino acid sequence is~~ encodes a truncated protein with respect to the geminivirus wild-type protein.

**64. (currently amended)** The method according to claim 63 wherein the mutated geminivirus ~~gene-derived~~ C1/AL1/AC1 polynucleotide sequence made an ineffective target of the geminivirus-induced post-transcriptional transgene silencing is ~~SEQ ID No 4~~ SEQ ID NO: 4.

**65. (currently amended)** The method according to claim 64, wherein the truncated protein is Rep-210 having the sequence of ~~SEQ ID No 5~~ SEQ ID NO: 5.

**66-67. (cancelled)**

**68. (previously presented)** The method according to claim 55, wherein the plants, plant tissues or cells thereof belong to a member selected from the group consisting of tomato, pepper, tobacco, squash, manioc, sweet potato, cotton, melon, potato, soybean, corn, wheat, sugar cane, bean, and beet.

**69. (currently amended)** The method according to claim 55, wherein the continuous homology between the mutated C1/AL1/AC1 polynucleotide sequence and the selected C1/AL1/AC1 polynucleotide sequence is less than or equal to 5 nucleotides.